IFWO

RAW SEQUENCE LISTING   DATE: 08/31/2004
PATENT APPLICATION: US/10/795,933   TIME: 12:53:28

        Input Set : N:\Crf3\RULE60\10795933.raw
        Output Set: N:\CRF4\08312004\J795933.raw

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 1 <110> APPLICANT: Zavada, Jan
 2         Pastorekova, Silvia
 3         Pastorek, Jaromir
 4 <120> TITLE OF INVENTION: MN Gene and Protein
 5 <130> FILE REFERENCE: D-0021-2
 6 <140> CURRENT APPLICATION NUMBER: US/10/795,933
 7 <141> CURRENT FILING DATE: 2004-03-08
 8 <150> PRIOR APPLICATION NUMBER: US/08/260,190
 9 <151> PRIOR FILING DATE: 1994-06-15
10 <150> PRIOR APPLICATION NUMBER: 08/177,093
11 <151> PRIOR FILING DATE: 1993-12-30
12 <150> PRIOR APPLICATION NUMBER: 07/964,589
13 <151> PRIOR FILING DATE: 1992-10-21
14 <150> PRIOR APPLICATION NUMBER: PV-709-92
15 <151> PRIOR FILING DATE: 1992-03-11
16 <160> NUMBER OF SEQ ID NOS: 26
17 <170> SOFTWARE: PatentIn Ver. 2.0
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 1399
21 <212> TYPE: DNA
22 <213> ORGANISM: HUMAN
23 <220> FEATURE:
24 <221> NAME/KEY: CDS
25 <222> LOCATION: (1)..(1266)
26 <400> SEQUENCE: 1
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28     Gln Arg Leu Pro Arg Met Gln Glu Asp Ser Pro Leu Gly Gly Gly Ser
29      1               5                  10                  15
30     tct ggg gaa gat gac cca ctg ggc gag gag gat ctg ccc agt gaa gag    96
31     Ser Gly Glu Asp Asp Pro Leu Gly Glu Glu Asp Leu Pro Ser Glu Glu
32                    20                  25                  30
33     gat tca ccc aga gag gag gat cca ccc gga gag gag gat cta cct gga   144
34     Asp Ser Pro Arg Glu Glu Asp Pro Pro Gly Glu Glu Asp Leu Pro Gly
35                35                  40                  45
36     gag gag gat cta cct gga gag gag gat cta cct gaa gtt aag cct aaa   192
37     Glu Glu Asp Leu Pro Gly Glu Glu Asp Leu Pro Glu Val Lys Pro Lys
38             50                  55                  60
39     tca gaa gaa gag ggc tcc ctg aag tta gag gat cta cct act gtt gag   240
40     Ser Glu Glu Glu Gly Ser Leu Lys Leu Glu Asp Leu Pro Thr Val Glu
41      65                  70                  75                  80
42     gct cct gga gat cct caa gaa ccc cag aat aat gcc cac agg gac aaa   288
43     Ala Pro Gly Asp Pro Gln Glu Pro Gln Asn Asn Ala His Arg Asp Lys
44                    85                  90                  95
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45   gaa ggg gat gac cag agt cat tgg cgc tat gga ggc gac ccg ccc tgg   336
46   Glu Gly Asp Asp Gln Ser His Trp Arg Tyr Gly Gly Asp Pro Pro Trp
47               100                 105                 110
48   ccc cgg gtg tcc cca gcc tgc gcg ggc cgc ttc cag tcc ccg gtg gat   384
49   Pro Arg Val Ser Pro Ala Cys Ala Gly Arg Phe Gln Ser Pro Val Asp
50               115                 120                 125
51   atc cgc ccc cag ctc gcc gcc ttc tgc ccg gcc ctg cgc ccc ctg gaa   432
52   Ile Arg Pro Gln Leu Ala Ala Phe Cys Pro Ala Leu Arg Pro Leu Glu
53               130                 135                 140
54   ctc ctg ggc ttc cag ctc ccg ccg ctc cca gaa ctg cgc ctg cgc aac   480
55   Leu Leu Gly Phe Gln Leu Pro Pro Leu Pro Glu Leu Arg Leu Arg Asn
56   145                 150                 155                 160
57   aat ggc cac agt gtg caa ctg acc ctg cct cct ggg cta gag atg gct   528
58   Asn Gly His Ser Val Gln Leu Thr Leu Pro Pro Gly Leu Glu Met Ala
59               165                 170                 175
60   ctg ggt ccc ggg cgg gag tac cgg gct ctg cag ctg cat ctg cac tgg   576
61   Leu Gly Pro Gly Arg Glu Tyr Arg Ala Leu Gln Leu His Leu His Trp
62               180                 185                 190
63   ggg gct gca ggt cgt ccg ggc tcg gag cac act gtg gaa ggc cac cgt   624
64   Gly Ala Ala Gly Arg Pro Gly Ser Glu His Thr Val Glu Gly His Arg
65               195                 200                 205
66   ttc cct gcc gag atc cac gtg gtt cac ctc agc acc gcc ttt gcc aga   672
67   Phe Pro Ala Glu Ile His Val Val His Leu Ser Thr Ala Phe Ala Arg
68               210                 215                 220
69   gtt gac gag gcc ttg ggg cgc ccg gga ggc ctg gcc gtg ttg gcc gcc   720
70   Val Asp Glu Ala Leu Gly Arg Pro Gly Gly Leu Ala Val Leu Ala Ala
71   225                 230                 235                 240
72   ttt ctg gag gag ggc ccg gaa gaa aac agt gcc tat gag cag ttg ctg   768
73   Phe Leu Glu Glu Gly Pro Glu Glu Asn Ser Ala Tyr Glu Gln Leu Leu
74               245                 250                 255
75   tct cgc ttg gaa gaa atc gct gag gaa ggc tca gag act cag gtc cca   816
76   Ser Arg Leu Glu Glu Ile Ala Glu Glu Gly Ser Glu Thr Gln Val Pro
77               260                 265                 270
78   gga ctg gac ata tct gca ctc ctg ccc tct gac ttc agc cgc tac ttc   864
79   Gly Leu Asp Ile Ser Ala Leu Leu Pro Ser Asp Phe Ser Arg Tyr Phe
80               275                 280                 285
81   caa tat gag ggg tct ctg act aca ccg ccc tgt gcc cag ggt gtc atc   912
82   Gln Tyr Glu Gly Ser Leu Thr Thr Pro Pro Cys Ala Gln Gly Val Ile
83               290                 295                 300
84   tgg act gtg ttt aac cag aca gtg atg ctg agt gct aag cag ctc cac   960
85   Trp Thr Val Phe Asn Gln Thr Val Met Leu Ser Ala Lys Gln Leu His
86   305                 310                 315                 320
87   acc ctc tct gac acc ctg tgg gga cct ggt gac tct cgg cta cag ctg   1008
88   Thr Leu Ser Asp Thr Leu Trp Gly Pro Gly Asp Ser Arg Leu Gln Leu
89               325                 330                 335
90   aac ttc cga gcg acg cag cct ttg aat ggg cga gtg att gag gcc tcc   1056
91   Asn Phe Arg Ala Thr Gln Pro Leu Asn Gly Arg Val Ile Glu Ala Ser
92               340                 345                 350
93   ttc cct gct gga gtg gac agc agt cct cgg gct gct gag cca gtc cag   1104
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      Input Set : N:\Crf3\RULE60\10795933.raw
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94       Phe Pro Ala Gly Val Asp Ser Ser Pro Arg Ala Ala Glu Pro Val Gln
95               355                 360                 365
96       ctg aat tcc tgc ctg gct gct ggt gac atc cta gcc ctg gtt ttt ggc   1152
97       Leu Asn Ser Cys Leu Ala Ala Gly Asp Ile Leu Ala Leu Val Phe Gly
98               370                 375                 380
99       ctc ctt ttt gct gtc acc agc gtc gcg ttc ctt gtg cag atg aga agg   1200
100      Leu Leu Phe Ala Val Thr Ser Val Ala Phe Leu Val Gln Met Arg Arg
101      385                 390                 395                 400
102      cag cac aga agg gga acc aaa ggg ggt gtg agc tac cgc cca gca gag    1248
103      Gln His Arg Arg Gly Thr Lys Gly Gly Val Ser Tyr Arg Pro Ala Glu
104              405                 410                 415
105      gta gcc gag act gga gcc tagaggctgg atcttggaga atgtgagaag          1296
106      Val Ala Glu Thr Gly Ala
107                  420
108      ccagccagag gcatctgagg gggagccggt aactgtcctg tcctgctcat tatgccactt 1356
109      cctttaact gccaagaaat tttttaaaat aaatatttat aat                    1399
111  <210> SEQ ID NO: 2
112  <211> LENGTH: 422
113  <212> TYPE: PRT
114  <213> ORGANISM: HUMAN
115  <400> SEQUENCE: 2
116      Gln Arg Leu Pro Arg Met Gln Glu Asp Ser Pro Leu Gly Gly Gly Ser
117      1                 5                   10                  15
118      Ser Gly Glu Asp Asp Pro Leu Gly Glu Glu Asp Leu Pro Ser Glu Glu
119              20                  25                  30
120      Asp Ser Pro Arg Glu Glu Asp Pro Pro Gly Glu Glu Asp Leu Pro Gly
121              35                  40                  45
122      Glu Glu Asp Leu Pro Gly Glu Glu Asp Leu Pro Glu Val Lys Pro Lys
123          50                  55                  60
124      Ser Glu Glu Glu Gly Ser Leu Lys Leu Glu Asp Leu Pro Thr Val Glu
125      65                  70                  75                  80
126      Ala Pro Gly Asp Pro Gln Glu Pro Gln Asn Asn Ala His Arg Asp Lys
127              85                  90                  95
128      Glu Gly Asp Asp Gln Ser His Trp Arg Tyr Gly Gly Asp Pro Pro Trp
129              100                 105                 110
130      Pro Arg Val Ser Pro Ala Cys Ala Gly Arg Phe Gln Ser Pro Val Asp
131              115                 120                 125
132      Ile Arg Pro Gln Leu Ala Ala Phe Cys Pro Ala Leu Arg Pro Leu Glu
133          130                 135                 140
134      Leu Leu Gly Phe Gln Leu Pro Pro Leu Pro Glu Leu Arg Leu Arg Asn
135      145                 150                 155                 160
136      Asn Gly His Ser Val Gln Leu Thr Leu Pro Pro Gly Leu Glu Met Ala
137              165                 170                 175
138      Leu Gly Pro Gly Arg Glu Tyr Arg Ala Leu Gln Leu His Leu His Trp
139              180                 185                 190
140      Gly Ala Ala Gly Arg Pro Gly Ser Glu His Thr Val Glu Gly His Arg
141              195                 200                 205
142      Phe Pro Ala Glu Ile His Val Val His Leu Ser Thr Ala Phe Ala Arg
143          210                 215                 220
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144      Val Asp Glu Ala Leu Gly Arg Pro Gly Gly Leu Ala Val Leu Ala Ala
145      225                 230                 235                 240
146      Phe Leu Glu Glu Gly Pro Glu Glu Asn Ser Ala Tyr Glu Gln Leu Leu
147                      245                 250                 255
148      Ser Arg Leu Glu Glu Ile Ala Glu Glu Gly Ser Glu Thr Gln Val Pro
149                      260                 265                 270
150      Gly Leu Asp Ile Ser Ala Leu Leu Pro Ser Asp Phe Ser Arg Tyr Phe
151                  275                 280                 285
152      Gln Tyr Glu Gly Ser Leu Thr Thr Pro Pro Cys Ala Gln Gly Val Ile
153          290                 295                 300
154      Trp Thr Val Phe Asn Gln Thr Val Met Leu Ser Ala Lys Gln Leu His
155      305                 310                 315                 320
156      Thr Leu Ser Asp Thr Leu Trp Gly Pro Gly Asp Ser Arg Leu Gln Leu
157                      325                 330                 335
158      Asn Phe Arg Ala Thr Gln Pro Leu Asn Gly Arg Val Ile Glu Ala Ser
159                  340                 345                 350
160      Phe Pro Ala Gly Val Asp Ser Ser Pro Arg Ala Ala Glu Pro Val Gln
161          355                 360                 365
162      Leu Asn Ser Cys Leu Ala Ala Gly Asp Ile Leu Ala Leu Val Phe Gly
163          370                 375                 380
164      Leu Leu Phe Ala Val Thr Ser Val Ala Phe Leu Val Gln Met Arg Arg
165      385                 390                 395                 400
166      Gln His Arg Arg Gly Thr Lys Gly Gly Val Ser Tyr Arg Pro Ala Glu
167                  405                 410                 415
168      Val Ala Glu Thr Gly Ala
169                  420
171 <210> SEQ ID NO: 3
172 <211> LENGTH: 29
173 <212> TYPE: DNA
174 <213> ORGANISM: HUMAN
175 <400> SEQUENCE: 3
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179 <211> LENGTH: 19
180 <212> TYPE: DNA
181 <213> ORGANISM: HUMAN
182 <400> SEQUENCE: 4
183      ggaatcctcc tgcatccgg                                         19
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186 <211> LENGTH: 1522
187 <212> TYPE: DNA
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189 <220> FEATURE:
190 <221> NAME/KEY: CDS
191 <222> LOCATION: (13)..(1389)
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194 <222> LOCATION: (124)..(1389)
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196   acagtcagcc gc atg gct ccc ctg tgc ccc agc ccc tgg ctc cct ctg ttg  51
197                 Met Ala Pro Leu Cys Pro Ser Pro Trp Leu Pro Leu Leu
198                     -35                 -30                 -25
199   atc ccg gcc cct gct cca ggc ctc act gtg caa ctg ctg ctg tca ctg    99
200   Ile Pro Ala Pro Ala Pro Gly Leu Thr Val Gln Leu Leu Leu Ser Leu
201                 -20                 -15                 -10
202   ctg ctt ctg atg cct gtc cat ccc cag agg ttg ccc cgg atg cag gag   147
203   Leu Leu Leu Met Pro Val His Pro Gln Arg Leu Pro Arg Met Gln Glu
204                 -5                  -1  1                   5
205   gat tcc ccc ttg gga gga ggc tct tct ggg gaa gat gac cca ctg ggc   195
206   Asp Ser Pro Leu Gly Gly Gly Ser Ser Gly Glu Asp Asp Pro Leu Gly
207            10                  15                  20
208   gag gag gat ctg ccc agt gaa gag gat tca ccc aga gag gag gat cca   243
209   Glu Glu Asp Leu Pro Ser Glu Glu Asp Ser Pro Arg Glu Glu Asp Pro
210      25                  30                  35                  40
211   ccc gga gag gag gat cta cct gga gag gag gat cta cct gga gag gag   291
212   Pro Gly Glu Glu Asp Leu Pro Gly Glu Glu Asp Leu Pro Gly Glu Glu
213                 45                  50                  55
214   gat cta cct gaa gtt aag cct aaa tca gaa gaa gag ggc tcc ctg aag   339
215   Asp Leu Pro Glu Val Lys Pro Lys Ser Glu Glu Glu Gly Ser Leu Lys
216                 60                  65                  70
217   tta gag gat cta cct act gtt gag gct cct gga gat cct caa gaa ccc   387
218   Leu Glu Asp Leu Pro Thr Val Glu Ala Pro Gly Asp Pro Gln Glu Pro
219                 75                  80                  85
220   cag aat aat gcc cac agg gac aaa gaa ggg gat gac cag agt cat tgg   435
221   Gln Asn Asn Ala His Arg Asp Lys Glu Gly Asp Asp Gln Ser His Trp
222            90                  95                  100
223   cgc tat gga ggc gac ccg ccc tgg ccc cgg gtg tcc cca gcc tgc gcg   483
224   Arg Tyr Gly Gly Asp Pro Pro Trp Pro Arg Val Ser Pro Ala Cys Ala
225   105                 110                 115                 120
226   ggc cgc ttc cag tcc ccg gtg gat atc cgc ccc cag ctc gcc gcc ttc   531
227   Gly Arg Phe Gln Ser Pro Val Asp Ile Arg Pro Gln Leu Ala Ala Phe
228                 125                 130                 135
229   tgc ccg gcc ctg cgc ccc ctg gaa ctc ctg ggc ttc cag ctc ccg ccg   579
230   Cys Pro Ala Leu Arg Pro Leu Glu Leu Leu Gly Phe Gln Leu Pro Pro
231                 140                 145                 150
232   ctc cca gaa ctg cgc ctg cgc aac aat ggc cac agt gtg caa ctg acc   627
233   Leu Pro Glu Leu Arg Leu Arg Asn Asn Gly His Ser Val Gln Leu Thr
234                 155                 160                 165
235   ctg cct cct ggg cta gag atg gct ctg ggt ccc ggg cgg gag tac cgg   675
236   Leu Pro Pro Gly Leu Glu Met Ala Leu Gly Pro Gly Arg Glu Tyr Arg
237            170                 175                 180
238   gct ctg cag ctg cat ctg cac tgg ggg gct gca ggt cgt ccg ggc tcg   723
239   Ala Leu Gln Leu His Leu His Trp Gly Ala Ala Gly Arg Pro Gly Ser
240   185                 190                 195                 200
241   gag cac act gtg gaa ggc cac cgt ttc cct gcc gag atc cac gtg gtt   771
242   Glu His Thr Val Glu Gly His Arg Phe Pro Ala Glu Ile His Val Val
243                 205                 210                 215
244   cac ctc agc acc gcc ttt gcc aga gtt gac gag gcc ttg ggg cgc ccg   819
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RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 08/31/2004
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Input Set : N:\Crf3\RULE60\10795933.raw
Output Set: N:\CRF4\08312004\J795933.raw

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:9; N Pos. 36,37,41,42,46,47
Seq#:19; N Pos. 7
Seq#:23; N Pos. 1974,2346
Seq#:25; Xaa Pos. 3,4
Seq#:26; Xaa Pos. 3,4

VERIFICATION SUMMARY   DATE: 08/31/2004
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Input Set : **N:\Crf3\RULE60\10795933.raw**
Output Set: **N:\CRF4\08312004\J795933.raw**

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L:373 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:9
L:373 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:0
L:457 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:19
L:457 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19 after pos.:0
L:527 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:23
L:527 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23 after pos.:1920
M:341 Repeated in SeqNo=23
L:597 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:25
L:597 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25 after pos.:0
L:608 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:26
L:608 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26 after pos.:0
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